A1 cont

of 31/1. Chromium release was measured 4 hours later. The asterisks indicate the mutated amino acids.

Please substitute the paragraph located on page 20, lines 3-12, with the following paragraph:

A2

T2 cells were incubated at 26°C for 16 hours in serum-free medium, with or without peptide at a concentration of 20μm. Next, the peptides (SEQ ID NOS. 2, 7, 1, and 8) were again added, and the cells were incubated at 37°C. At 30-minute or one-hour intervals, the cell pellets were collected and the change in HLA-A2 expression was analyzed by flow cytometry with an anti-HLA-A2 mAb (MA2.1). The amino acid sequences of the peptides are represented. The mutated amino acid is represented by an asterisk.

Please substitute the paragraph on page 23, lines 2-23, with the following paragraph:

A3

In order to delimit the minimum nucleotide region encoding the antigenic peptide, multiple truncated cDNAs were obtained from the A18 cDNA clone. The use of exonuclease III made it possible to gradually generate deletions starting from the 3' end of the cDNA (Figure 5). These cDNA fragments were cotransfected into COS-7 cells with the autologous HLA-A*0201 cDNA. A minimum coding nucleotide region was located between nucleotides 730 and 944. The truncation in the region carrying the single mutation specific for the tumor abolishes recognition by 11C2 CTLs. Peptides carrying the HLAS-A*0201 binding motif were sought in this region, and among the 18 peptides assayed, only 2 (the nonapeptide SLFEGIDIY (SEQ ID NO: 1), amino acids 286 to 294, and the decapeptide SLFEGIDIYT (SEQ ID NO: 2), amino acids 286 to 295)

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